Proceedings of AMIA Annual Symposium 2002:978.

GenNav: Visualizing Gene Ontology as a graph

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Most browsers available for visualizing and navigating the Gene Ontology™[1] display its polyhierarchical structure as a list of indented concepts. Figure 1 partially shows, for example, how the AmiGO browser[2] visualizes the concept *extrinsic plasma membrane protein*. As a result, although all the information needed to transform this representation into a graph structure is present, we argue that the cognitive effort required to do this transformation is probably unnecessary.

In a previous experiment, we developed strategies for visualizing complex, polyhierarchical structures drawn from the Unified Medical Language System® (UMLS®), and found directed acyclic graphs (DAGs) to provide suitable representations. This experiment resulted in the development of an application: the UMLS Semantic Navigator[3], based, in part, on the graph visualization package GraphViz[4].

[1] www.geneontology.org
[2] godatabase.org/cgi-bin/go.cgi
[3] umlsks.nlm.nih.gov → Resources → Semantic Navigator
[4] www.research.att.com/sw/tools/graphviz/

Applying the same techniques to the visualization of polyhierarchical structures from Gene Ontology, we developed GenNav. Figure 2 shows an example of the graphs produced by GenNav. In this example, the concepts used to annotate the gene *Dystrophin* include the cellular component *extrinsic plasma membrane protein*, also represented displayed in Figure 1, so the representation of this concept can be compared across the two figures.

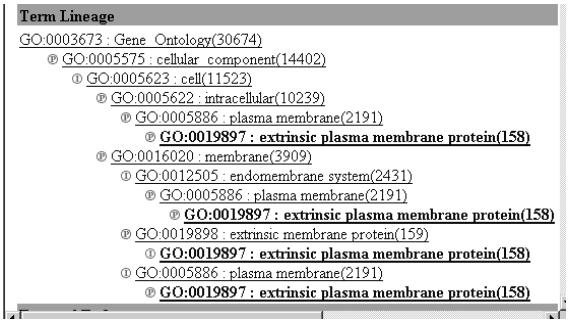

Figure 1 – The AmiGO browser.

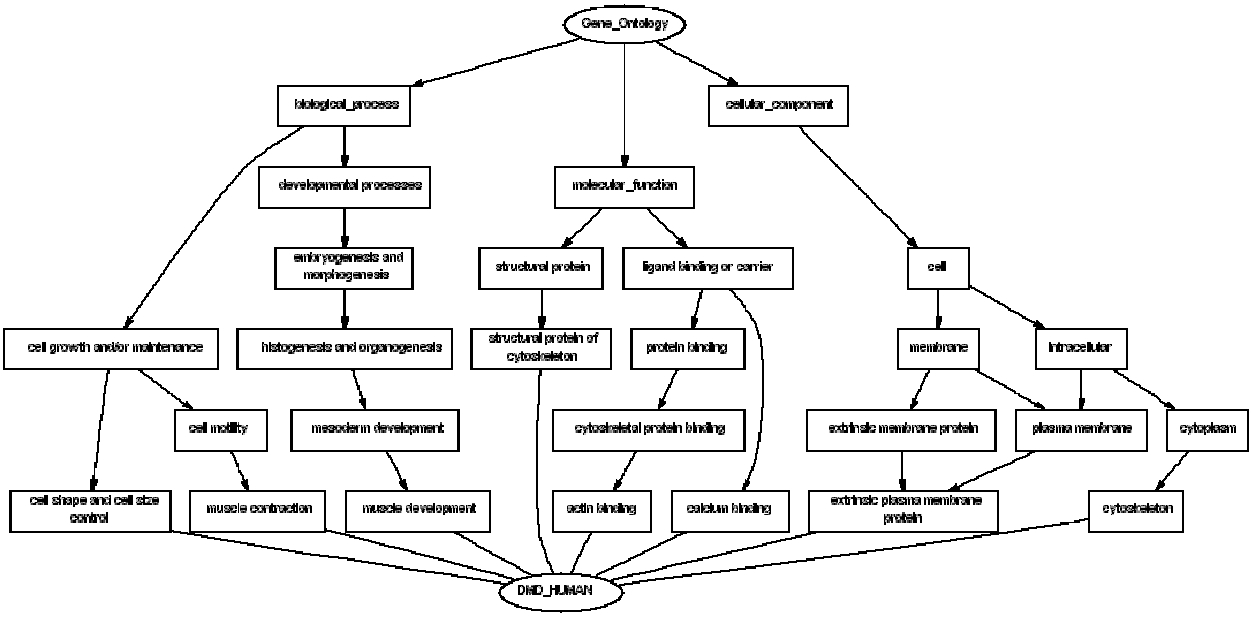

Figure 2 - Graph of the concepts related to "dystrophin" (DMD_HUMAN) in Gene Ontology.